

Disclosed are methods for identifying nucleic acids in a sample of nucleic acids in which nucleic acids are initially present in unequal amounts. The methods include partitioning the starting population of nucleic acids to form one or more subpopulations, and then identifying nucleic acids that are present in different amounts in the partitioned nucleic acid sample as compared to the starting population. Also disclosed are methods of generating databases based on sizes of DNA fragments and size-based sequencing of those fragments.

$\frac{1}{\sqrt{2}} \begin{pmatrix} 0 & -1 \\ 1 & 0 \end{pmatrix}$